



A circular map of the pCGN10800 plasmid, which is 19258 bp in size. The map shows various restriction enzyme sites labeled around the perimeter, such as PvuII 121, EcoRI 296, SacI 306, NcoI 346, StuI 486, NcoI 736, EcoRV 1444, BamHI 1659, NotI 1666, StuI 1837, StuI 1990, StuI 2482, EcoRV 2554, XhoI 2748, PstI 2863, and SacI 2869. Internal features include the RB (Replication Origin), polylinker, aadA, d35S, Turbo polylinker, ATPT2, tml 3' gene, 35S promoter, Tn5 kan gene, another tml 3' gene, LB (Lytic Bacteriophage), Spc/Str (Streptomycin/Spectinomycin resistance), and aacC1. Other labels include XhoI 13882, PvuI 14525, PvuI 15097, ClaI 15097, EcoRV 15111, SacI 15209, BglIII 16762, EcoRV 16958, and PvuI 13451.

Figure 2

A circular map of the pCGN10801 plasmid, which is 19788 bp in size. The map displays various restriction enzyme sites as short vertical lines radiating from the circle, each labeled with its name and position number. Key genetic features are indicated by arrows or specific symbols: RB (Right Border), aadA (ampicillin resistance gene), aacC1 (aminoglycoside acetyltransferase), Napin Promoter, Turbo linker, ATPT2, Napin 3', 35S promoter, Tn5 kan gene, tml 3' (tetM), LB (Left Border), ori pRi (replication origin for *Rhodospirillum rubrum*), Spc/Str (spectinomycin/streptomycin resistance), and XbaI site.

Restriction Enzyme Site (Position)
PvuII 121
EcoRI 296
SacI 306
SacI 645
EcoRV 1549
XbaI 1578
EcoRI 1773
Sall 2075
PstI 2085
XhoI 2192
EcoRV 2390
StuI 2462
StuI 2954
StuI 3107
NciI 3274
BamHI 3281
XhoI 3286
BamHI 3603
EcoRV 4447
PvuII 4646
PvuI 4677
XhoI 4726
PvuII 4962
EcoRV 5257
Sall 5467
EcoRI 5479
PvuII 5734
NciI 6060
EcoRI 6469
SmaI 6476
XhoI 7618
PvuI 7628
DraI 8080
PvuI 8164
XhoI 8609
SmaI 8773
EcoRV 8804
EcoRV 8976
EcoRV 9266
PvuII 9916
EcoRV 10115
BglIII 10246
XhoI 10302
PvuI 10332
Sall 10367
EcoRV 11004
NciI 11060
PvuII 11154
PvuI 11403
EcoRI 11543
EcoRI 11691
SmaI 12021
BglIII 12036
SacI 12059
PvuII 12171
PvuI 12306
XhoI 12814
BglIII 13425
PvuII 13697
SacI 13707
DraI 13826
PvuI 13981
XhoI 14412
PvuI 15055
PvuI 15627
ClaI 15627
EcoRV 15641
SacI 15739
BglIII 17292
EcoRV 17488

Figure 3

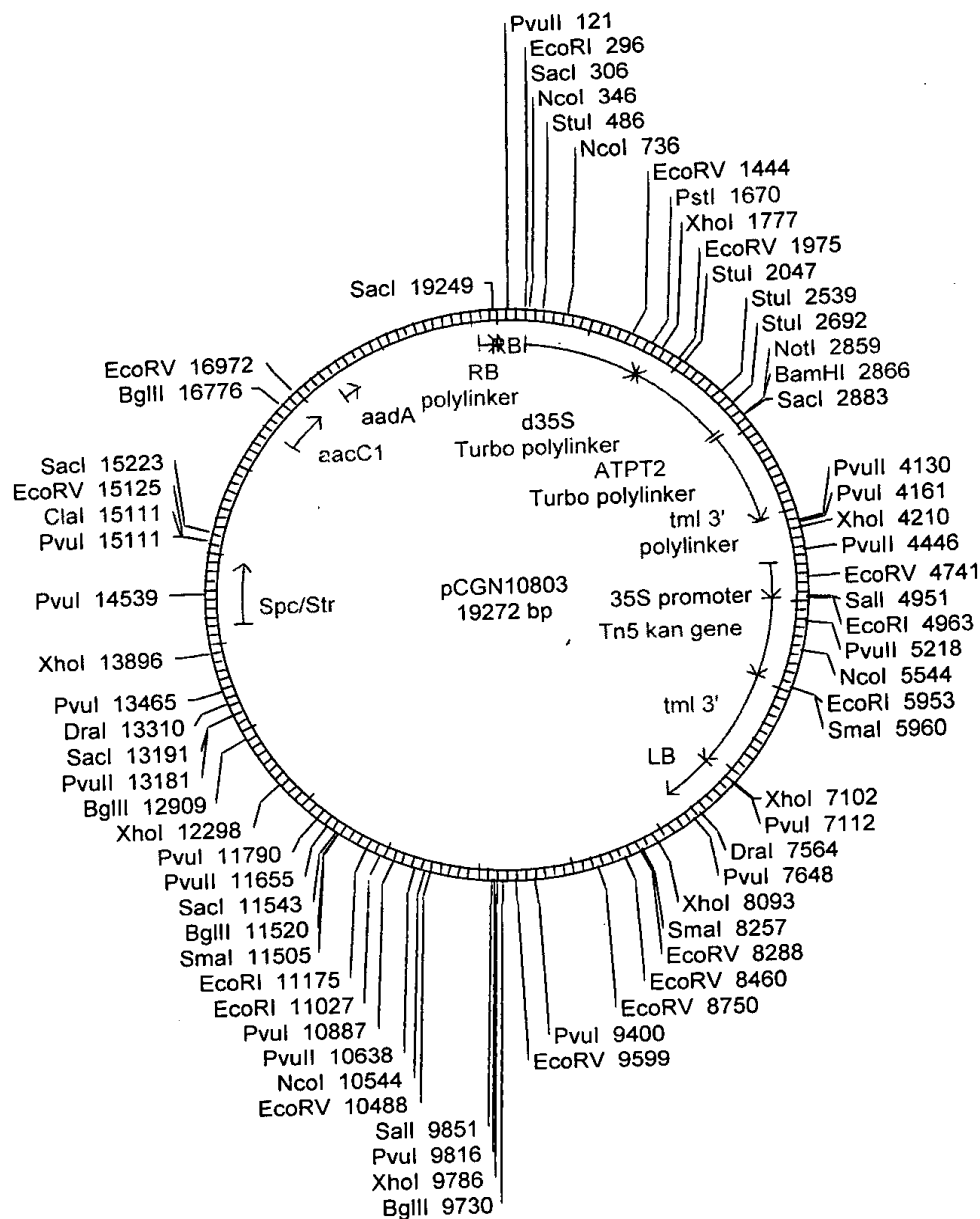


Figure 4

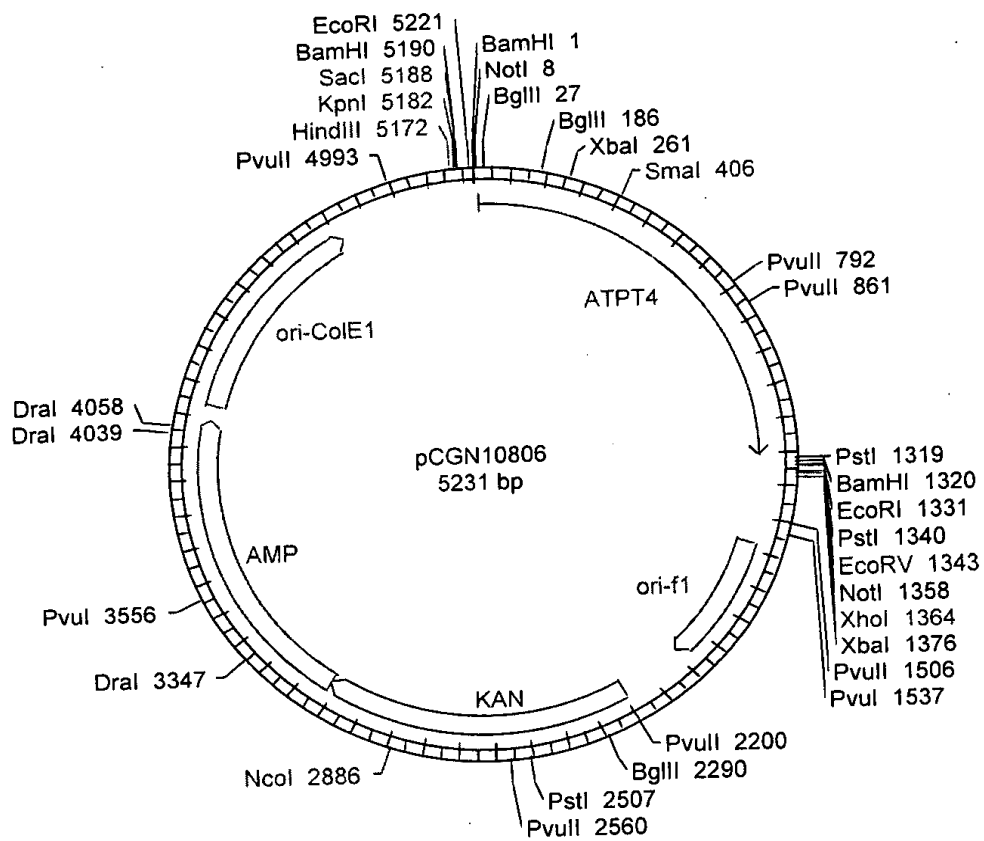


Figure 5

001101-03065500





A circular map of the pCGN10809 plasmid, which is 19300 bp in size. The map displays various restriction enzyme sites and genetic features. Key elements include:

- Restriction Sites:** Numerous sites are labeled with their respective enzymes and positions, such as PvuII 121, EcoRI 296, SacI 306, NcoI 346, StuI 486, NcoI 736, EcoRV 1444, BamHI 1659, NotI 1666, HindIII 2010, HindIII 2060, DraI 2161, PstI 2331, PstI 2503, HindIII 2660, BglII 2725, PvuII 2795, PstI 2822, PstI 2905, SacI 2911, PvuII 4158, PvuI 4189, XhoI 4238, PvuII 4474, EcoRV 4769, SalI 4979, EcoRI 4991, PvuII 5246, NcoI 5572, EcoRI 5981, SmaI 5988, XhoI 7130, PvuI 7140, PvuI 7676, XhoI 8121, SmaI 8285, EcoRV 8316, EcoRV 8488, EcoRV 8778, PvuI 9428, EcoRV 9627, EcoRV 10516, NcoI 10572, PvuI 10666, PvuI 10915, EcoRI 11055, EcoRI 11203, SmaI 11533, BglII 11548, SacI 11571, PvuII 11683, PvuI 11818, XhoI 12326, BglII 12937, PvuII 13209, SacI 13219, DraI 13338, PvuI 13493, XhoI 13924, PvuI 14567, PvuI 15139, ClaI 15139, EcoRV 15153, SacI 15251, BglII 16804, EcoRV 17000, and SacI 19277.
- Genetic Features:** The map includes a polylinker region with sites for aadA, aacC1, d35S, Turbo polylinker, ATPT3, tml 3', and a 35S promoter. It also features a Tn5 kan gene, a Spc/Str resistance gene, and a tml 3' gene.
- Other Labels:** The plasmid is labeled pCGN10809 and 19300 bp. Other labels include RB, BI, and LB.

Figure 8



**pCGN10810**  
19830 bp

**Genes and Features:**  
 aadA  
 aacC1  
 polylinker  
 Napin Promoter  
 Turbo linker  
 ATPT3  
 Turbo linker  
 Napin 3'  
 35S promoter  
 Tn5 kan gene  
 tml 3'  
 LB  
 ori pRi  
 Spc/Str

**Restriction Enzyme Sites (Clockwise from top):**  
 PvuII 121  
 EcoRI 296  
 SacI 306  
 SacI 645  
 EcoRV 1549  
 XbaI 1578  
 EcoRI 1773  
 SalI 2075  
 PstI 2085  
 PstI 2168  
 PvuII 2191  
 BglII 2257  
 HindIII 2322  
 PstI 2487  
 PstI 2659  
 DraI 2825  
 HindIII 2922  
 HindIII 2972  
 NotI 3316  
 BamHI 3323  
 XhoI 3328  
 BamHI 3645  
 EcoRV 4489  
 PvuII 4688  
 PvuI 4719  
 XhoI 4768  
 PvuII 5004  
 EcoRV 5299  
 SalI 5509  
 EcoRI 5521  
 PvuII 5776  
 NcoI 6102  
 EcoRI 6511  
 SmaI 6518  
 XhoI 7660  
 PvuI 7670  
 DraI 8122  
 PvuI 8206  
 XhoI 8651  
 SmaI 8815  
 EcoRV 8846  
 EcoRV 9018  
 EcoRV 9308  
 PvuI 9958  
 EcoRV 10157  
 BglII 10288  
 XhoI 10344  
 PvuI 10374  
 SalI 10409  
 EcoRV 11046  
 NcoI 11102  
 PvuII 11196  
 PvuI 11445  
 EcoRI 11585  
 EcoRI 11733  
 SmaI 12063  
 BglII 12078  
 SacI 12101  
 PvuII 12213  
 PvuI 12348  
 XhoI 12856  
 BglII 13467  
 PvuII 13739  
 SacI 13749  
 DraI 13868  
 PvuI 14023  
 XhoI 14454  
 PvuI 15097  
 PvuI 15669  
 ClaI 15669  
 EcoRV 15683  
 SacI 15781  
 BglII 17334  
 EcoRV 17530  
 SacI 19807

Figure 9

A circular map of the plasmid pCGN10811, which is 19830 bp in size. The map displays various restriction enzyme sites as short vertical lines radiating from the circle, each labeled with its name and position number. Key genetic features are indicated by arrows or specific labels around the perimeter, including the aadA gene, aacC1 gene, Spc/Str resistance genes, RB (Right Border), polylinker regions, Napin Promoter, Turbo linker, ATPT3, Napin 3', 35S promoter, Tn5 kan gene, tml 3' gene, and LB (Left Border). The map also shows several other genes like aadA and aacC1.

Restriction Enzyme	Position (bp)
PvuII	121
EcoRI	296
SacI	306
SacI	645
EcoRV	1549
XbaI	1578
EcoRI	1773
BamHI	2080
NciI	2087
HindIII	2431
HindIII	2481
DraI	2582
PstI	2752
PstI	2924
HindIII	3081
BglII	3146
PvuII	3216
PstI	3243
PstI	3326
BamHI	3645
EcoRV	4489
PvuII	4688
PvuI	4719
XhoI	4768
PvuII	5004
EcoRV	5299
Sall	5509
EcoRI	5521
PvuII	5776
NcoI	6102
EcoRI	6511
SmaI	6518
XhoI	7660
PvuI	7670
DraI	8122
PvuI	8206
XhoI	8651
SmaI	8815
EcoRV	8846
EcoRV	9018
EcoRV	9308
PvuII	9958
EcoRV	10157
BglII	10288
XhoI	10344
PvuI	10374
Sall	10409
EcoRV	11046
NcoI	11102
PvuII	11196
PvuI	11445
EcoRI	11585
EcoRI	11733
SmaI	12063
BglII	12078
SacI	12101
PvuII	12213
PvuI	12348
XhoI	12856
BglII	13467
PvuII	13739
SacI	13749
DraI	13868
PvuI	14023
XhoI	14454
PvuI	15097
PvuI	15669
Clal	15669
EcoRV	15683
SacI	15781
BglII	17334
EcoRV	17530
SacI	19807

Figure 10



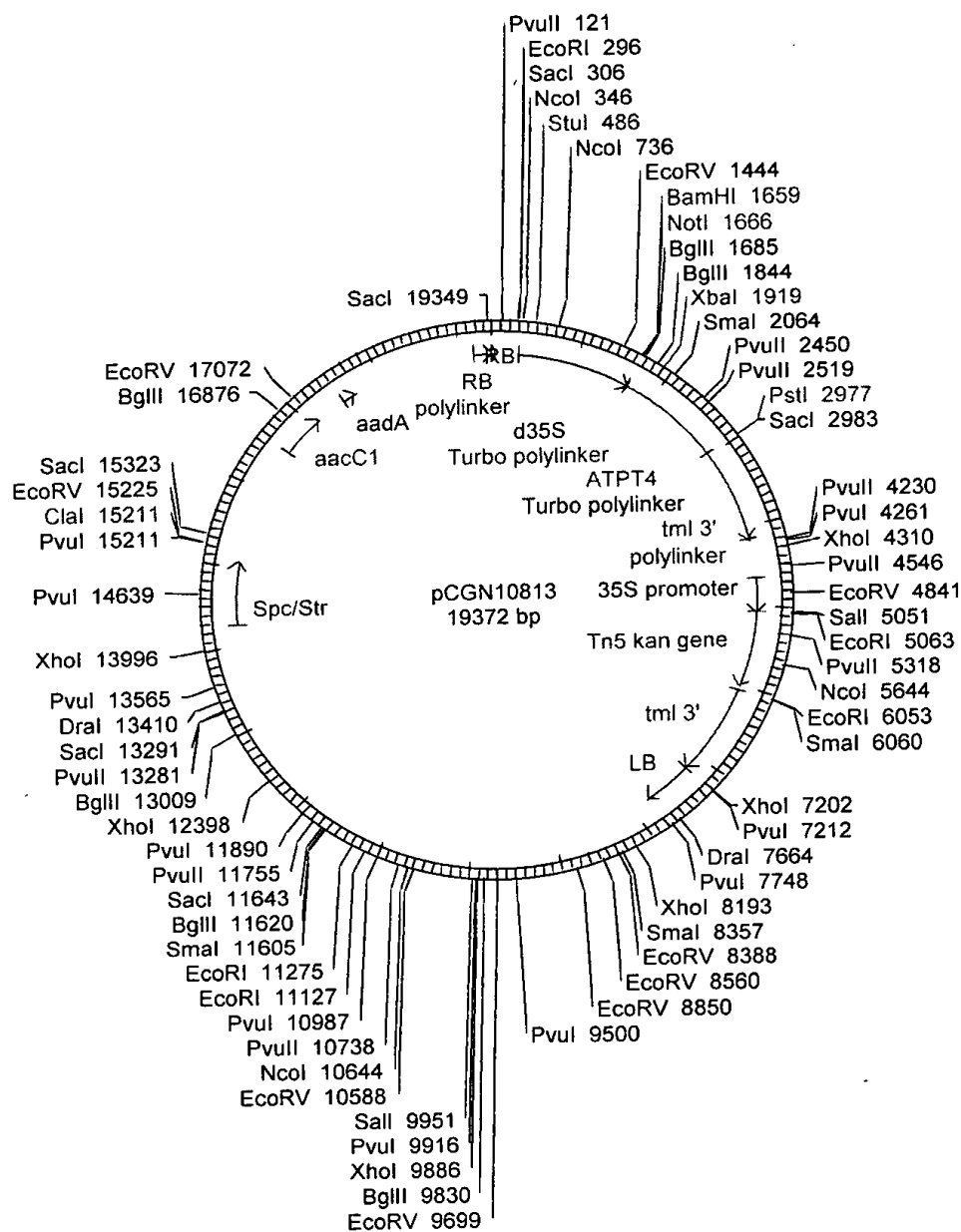


Figure 12

A circular map of the plasmid pCGN10814, which is 19902 bp in size. The map displays various restriction enzyme sites as short vertical lines radiating from the circle, each labeled with its name and position number. Key genetic features are indicated by arrows or asterisks around the perimeter, including the origin of replication (ori pRi), multiple antibiotic resistance genes (aadA, aacC1, Tn5 kan gene), promoters (Napin Promoter, ATPT4, 35S promoter), and other elements like the Spc/Str resistance marker and polylinker regions. The map is divided into segments by these features, with some segments containing specific restriction sites.

Restriction Enzyme	Position (bp)
PvuII	121
EcoRI	296
SacI	306
SacI	645
EcoRV	1549
XbaI	1578
EcoRI	1773
Sall	2075
PstI	2085
PvuII	2539
PvuII	2608
SmaI	2994
XbaI	3135
BglIII	3210
BglIII	3369
NotI	3388
BamHI	3395
XhoI	3400
BamHI	3717
EcoRV	4561
PvuII	4760
PvuI	4791
XhoI	4840
PvuII	5076
EcoRV	5371
Sall	5581
EcoRI	5593
PvuII	5848
NcoI	6174
EcoRI	6583
SmaI	6590
XhoI	7732
PvuI	7742
DraI	8194
PvuI	8278
XhoI	8723
SmaI	8887
EcoRV	8918
EcoRV	9090
EcoRV	9380
PvuI	10030
EcoRV	10229
BglIII	10360
XhoI	10416
PvuI	10446
Sall	10481
EcoRV	11118
NcoI	11174
PvuII	11268
PvuI	11517
EcoRI	11657
EcoRI	11805
SmaI	12135
BglIII	12150
SacI	12173
PvuII	12285
PvuI	12420
XhoI	12928
BglIII	13539
PvuI	13811
SacI	13821
DraI	13940
PvuI	14095
XhoI	14526
PvuI	15169
PvuI	15741
Clal	15741
EcoRV	15755
SacI	15853
BglIII	17406
EcoRV	17602
SacI	19879

Figure 13

A circular map of the pCGN10815 plasmid, which is 19902 bp in size. The map displays various restriction enzyme sites and genetic features. Key elements include:

- Restriction Sites:** Numerous sites are labeled around the circle, including EcoRV, BglII, XbaI, SacI, PvuII, PstI, BamHI, EcoRI, NotI, BglIII, XhoI, SmaI, PvuI, ClaI, DraI, SalI, NcoI, and XbaI.
- Genetic Features:** The map identifies several functional regions:
  - polylinker** regions for cloning.
  - Napin Promoter** and **Turbo linker** sequences.
  - ATPT4** gene.
  - 35S promoter** and **Tn5 kan gene**.
  - tm1 3'** and **LB** (Lysogenic Bacteriophage) regions.
  - aadA** and **aacC1** antibiotic resistance genes.
  - Spc/Str** (Spectinomycin/Streptomycin) resistance region.
  - RB** (Right Border) and **LB** (Left Border) sequences.
- Other Labels:** The map also includes labels for **pCGN10815** and **19902 bp**.

Figure 14







001101-65066960

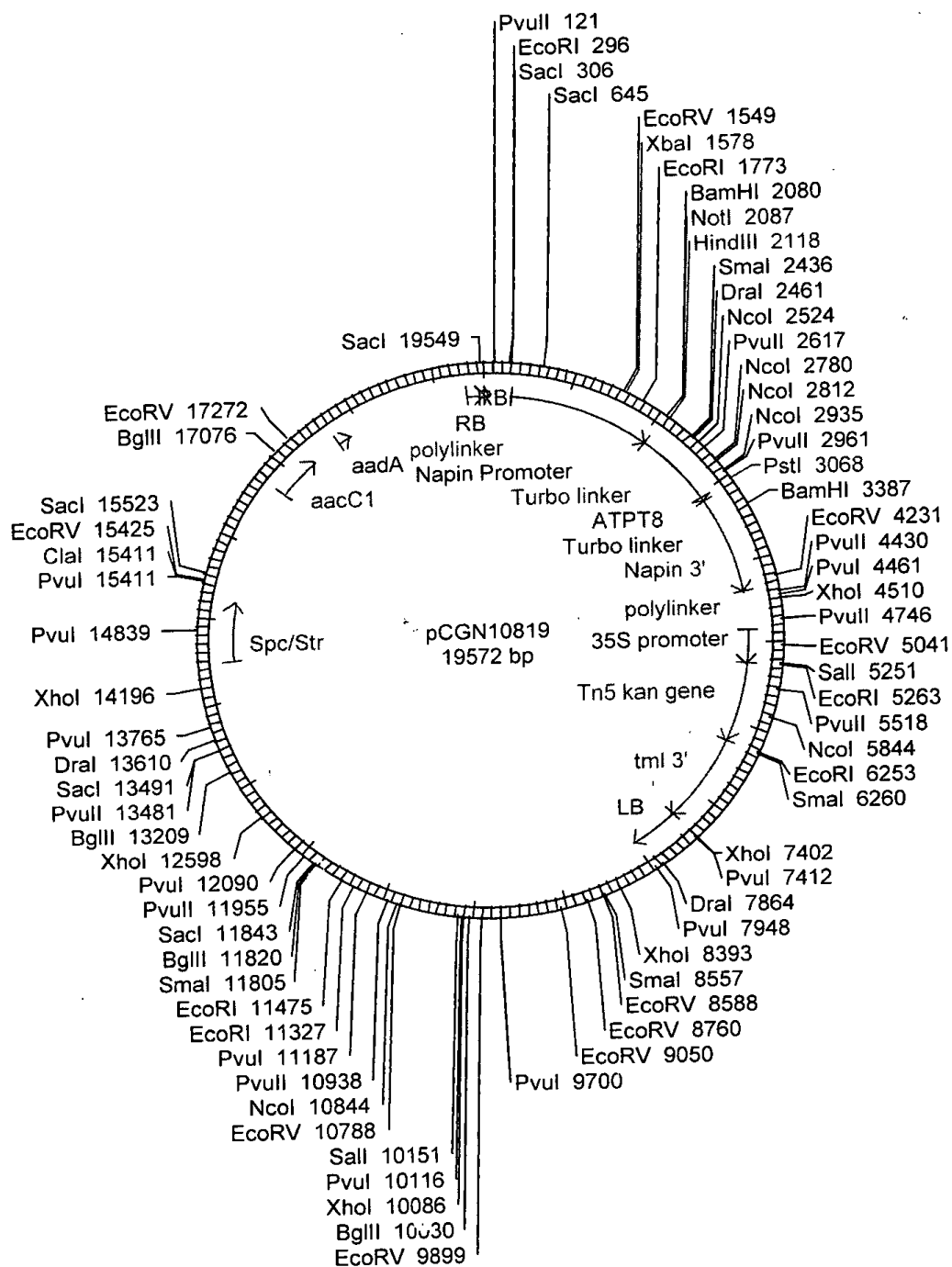


Figure 17

A circular map of the pCGN10824 plasmid, which is 19240 bp in size. The map displays various restriction enzyme sites and genetic features. Key elements include:

- Restriction Sites:** Numerous sites are labeled around the circle, including EcoRI, SacI, NcoI, StuI, PvuII, EcoRV, BamHI, NotI, PstI, DraI, SmaI, XhoI, SalI, BglII, ClaI, and PvuI.
- Genetic Features:** The map identifies several functional regions:
  - polylinker:** Located near the top, flanked by RB (Right Border) and LB (Left Border) sequences.
  - aadA:** An aminoglycoside resistance gene.
  - aacC1:** A tetracycline resistance gene.
  - d35S:** A 35S promoter.
  - Tn5 kan gene:** A tetracycline resistance gene.
  - ATPT12:** A transcription start site.
  - 35S promoter:** A promoter for the Tn5 kan gene.
  - tm1 3':** A transcription start site for the Tn5 kan gene.
  - Spc/Str:** A streptomycin resistance gene.
- Plasmid Size:** The total size is indicated as 19240 bp.

Figure 18

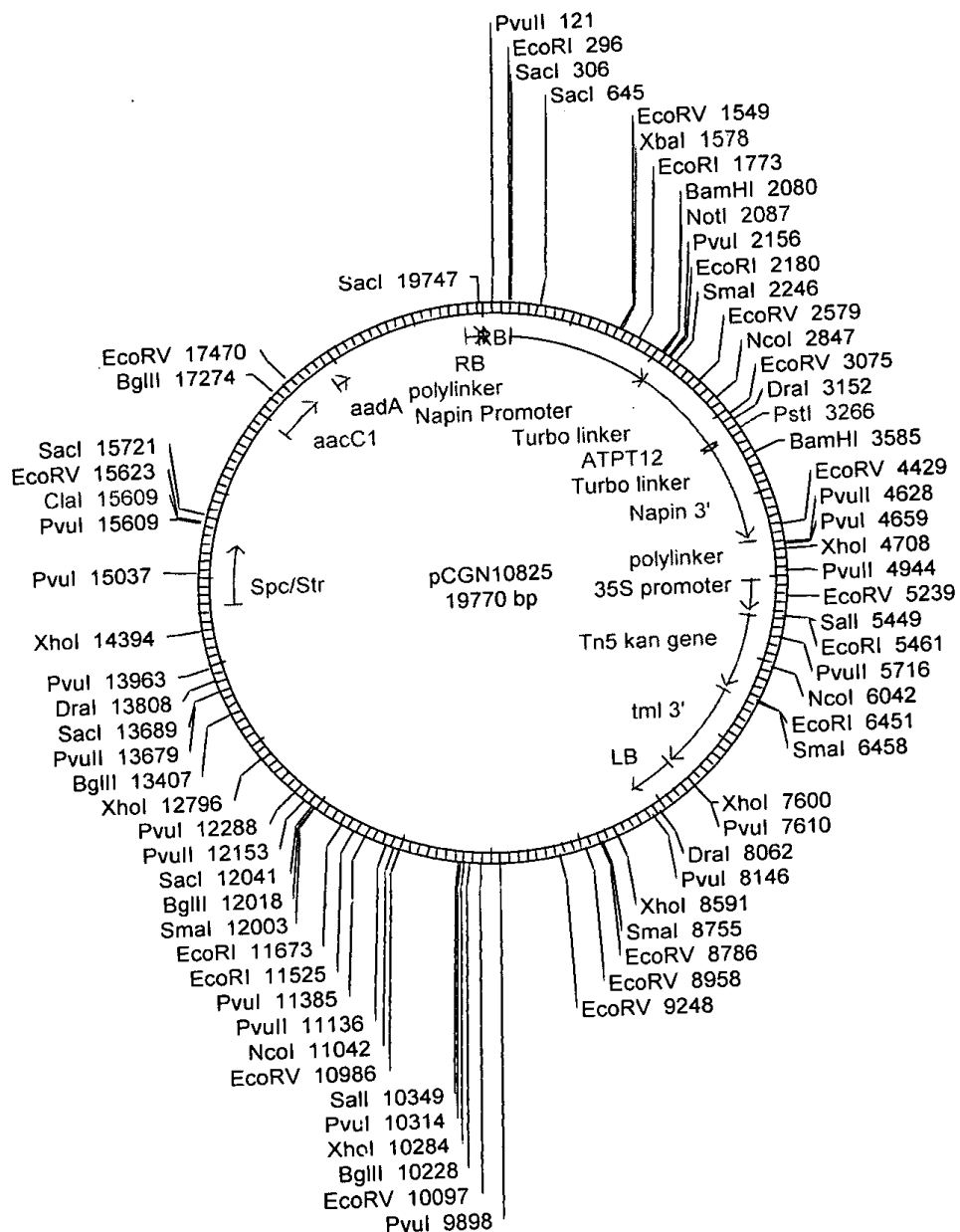


Figure 19

00111-0302500

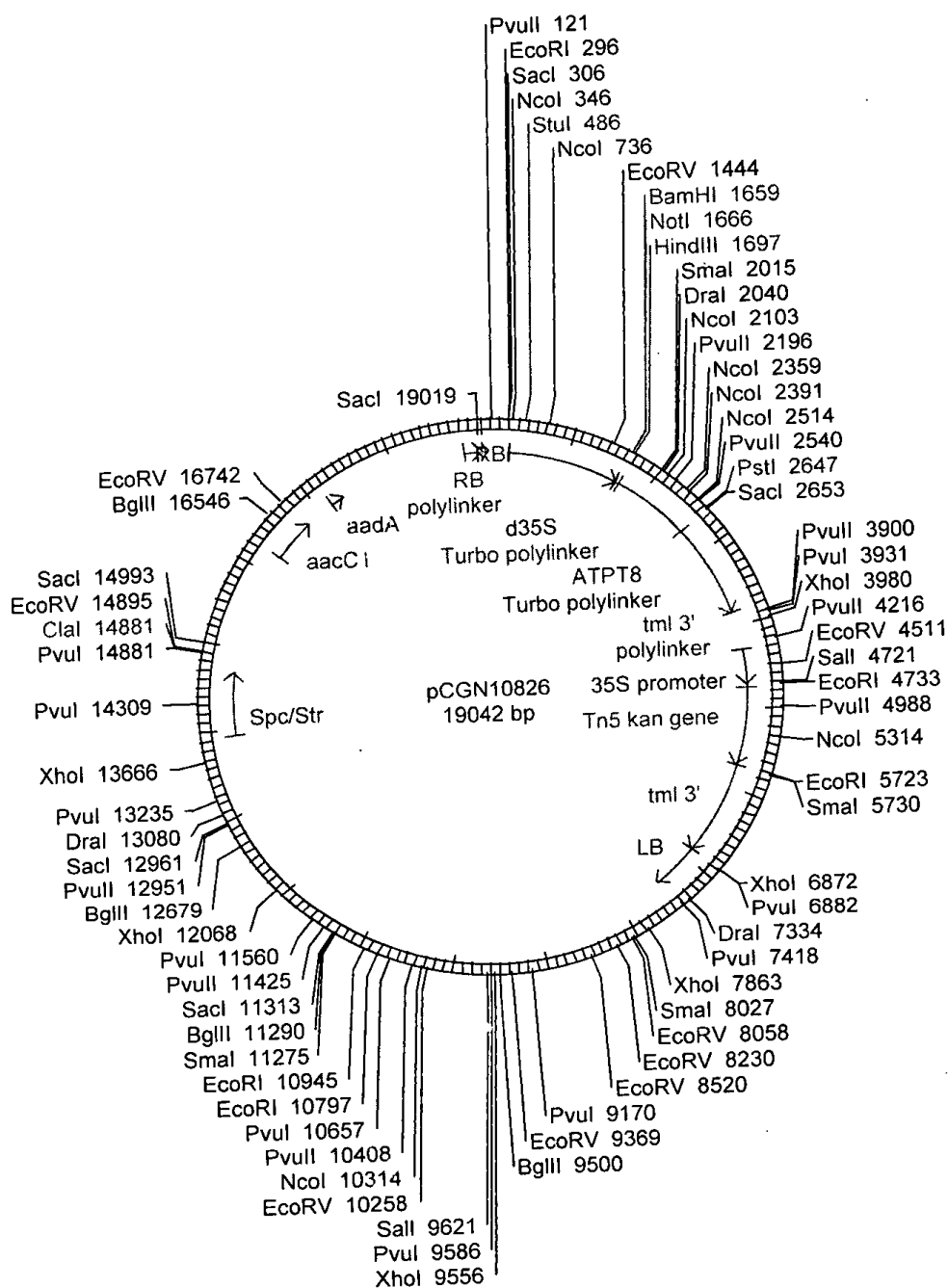


Figure 20



ATPT2 : ----- \* 20 \* 40 \* 60 \* 80  
 SLR1736 : ----- MESLSSSLVSAAGFCWKONLKLHSLSEIRVLCDSSKVAKPKFRNNLVPRDGGSSLLYPKHKSFRVNATAG : 80  
 ATPT3 : ----- MAFFGLSRVSRLLKSSVTPSSSSALLQSHSLNPVTHYNPTKCYPSWNNQVWSKREIHQKEFGVGNRYLICGSSS : 89  
 SLR0926 : ----- MRRSVYRFSSRISVSSSLPNRLLPWSRELCVANSFSQP ----- PVSTESTAKLGTIGVRSNDANRVATA : 67  
 ATPT4 : ----- MRRSVYRFSSRISVSSSLPNRLLPWSRELCVANSFSQP ----- PVSTESTAKLGTIGVRSNDANRVATA : 67  
 SLR1899 : ----- MRRSVYRFSSRISVSSSLPNRLLPWSRELCVANSFSQP ----- PVSTESTAKLGTIGVRSNDANRVATA : 67  
 ATPT12 : ----- MTSILNTVSTIHSSRVTSDVRGVLIRNSDVEFT ----- RRRSGSTLIYESPGRRFVRAAETDT : 63  
 SLR0056 : ----- MTSILNTVSTIHSSRVTSDVRGVLIRNSDVEFT ----- RRRSGSTLIYESPGRRFVRAAETDT : 63  
 ATPT8 : ----- MTSILNTVSTIHSSRVTSDVRGVLIRNSDVEFT ----- RRRSGSTLIYESPGRRFVRAAETDT : 63  
 SLR1518 : ----- MTSILNTVSTIHSSRVTSDVRGVLIRNSDVEFT ----- RRRSGSTLIYESPGRRFVRAAETDT : 63

ATPT2 : ----- \* 100 \* 120 \* 140 \* 160 \* 1  
 SLR1736 : ----- PEAFLDSNSKOK ----- SFRDSFPAFYR ----- FSRPHTIGTIVLSILS ----- VSEFLAVEKVS ----- DISPLFTGILE : 140  
 ATPT3 : ----- SSVLEGRPKKDDKEKSDGVVKKASW ----- MATQAFWR ----- FSRPHTIGTIVLSILS ----- VSEFLAVEKVS ----- DISPLFTGILE : 140  
 SLR0926 : ----- MVAQTPSSP ----- EISSRAALAGGHHYAR ----- LRMHHPAGELIMIPAWA ----- VCLAAQ ----- G ----- LPPLPLGITAL : 56  
 ATPT4 : ----- TAAATATATG ----- EISSRAALAGGHHYAR ----- LRMHHPAGELIMIPAWA ----- VCLAAQ ----- G ----- LPPLPLGITAL : 56  
 SLR1899 : ----- TKIHRQHDMSG ----- AVCKSYOULTKP ----- RIPLIITTAASMI ----- ASEGR ----- VDLPKLITLIG : 60  
 ATPT12 : ----- DKVKSQTPDKAP ----- AGGSSINOLLGKAS ----- QENNKWKIRNOLTKPVWPPLVWGVCGAASGNFHWTEPDVAKSILC : 139  
 SLR0056 : ----- QNT-GONQAKA ----- ROLLGKGAAP ----- GESSIMKIRIOLMKPIWIPLIWGVCGAASGGYIWSVEDFLKALTC : 73  
 ATPT8 : ----- EVPKLASAEY ----- FKRGGOKOF ----- RSTILMATALNVRP ----- EALIGEST ----- DIVTSELVROR : 63  
 SLR1518 : ----- SPLAPSTAPAT ----- RKLWJALIKP ----- PMYVAVVPIVIG ----- SAVAYGLTG ----- QWHGDVFTIFLL : 59

ATPT2 : ----- \* 80 \* 200 \* 220 \* 240 \* 260  
 SLR1736 : ----- AVFAALMMNIYIVG ----- QISIVEKVNKPYPILASGEYSVNTGIAIVASF ----- MSFWLGIWIGSWPLFWALF ----- SEMIGTAYS ----- INPLLR : 228  
 ATPT3 : ----- GALT ----- LRGAGCT ----- D ----- L ----- OD ----- FTKVDRTKLRPIASGLLT ----- PFOGIGFLG ----- QLLILG ----- ILQLNYSRYLGAS ----- SLLAVE : 246  
 SLR0926 : ----- GTLA ----- TSGLGCV ----- D ----- M ----- RD ----- POKERTKORPLAARALS ----- VQVGIGVAL ----- LALICAG ----- LAFLYLP ----- SFMLCVA ----- AVPIV : 132  
 ATPT4 : ----- TML ----- AASANS ----- O ----- FEISN ----- SKWKRTMLRPLPSGRISVPHAVAMATIASGACL ----- LASKTNM ----- AAGLASAN ----- LVLYAF : 215  
 SLR1899 : ----- GTFA ----- AASQOT ----- C ----- Y ----- OD ----- YEMLRTRARIPACKQOPRHALLFALA ----- GVLSEFAL ----- LATFVNV ----- SGCLALSG ----- IVFYML : 137  
 ATPT12 : ----- MM ----- SGFCITGYOT ----- DM ----- Y ----- RD ----- YEMLRTRARIPACKQOPRHALLFALA ----- GVLSEFAL ----- LATFVNV ----- SGCLALSG ----- IVFYML : 137  
 SLR0056 : ----- ML ----- SGPLMTGYOT ----- DEFY ----- RD ----- YEMLRTRARIPACKQOPRHALLFALA ----- GVLSEFAL ----- LATFVNV ----- SGCLALSG ----- IVFYML : 137  
 ATPT8 : ----- GIAE ----- ITEMHVASL ----- H ----- DV ----- L ----- ADATRGVGSINVMGNKMSVLADDEL ----- SRACGAL ----- AALKNTE ----- VALLATAVEHLVTGETM : 144  
 SLR1518 : ----- SAFA ----- IIAWINIS ----- D ----- F ----- SDTGIDVRKAHSVNLGNRNLYFLISNEFFL ----- AGVILGMSMS ----- WRAQDMT ----- LLEL ----- GVA ----- IFLGY : 138

Figure 22 1/2

00000000 10111111

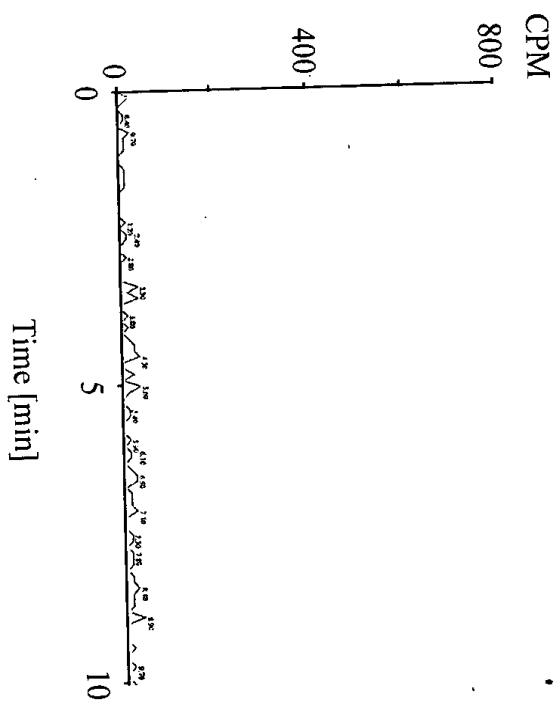
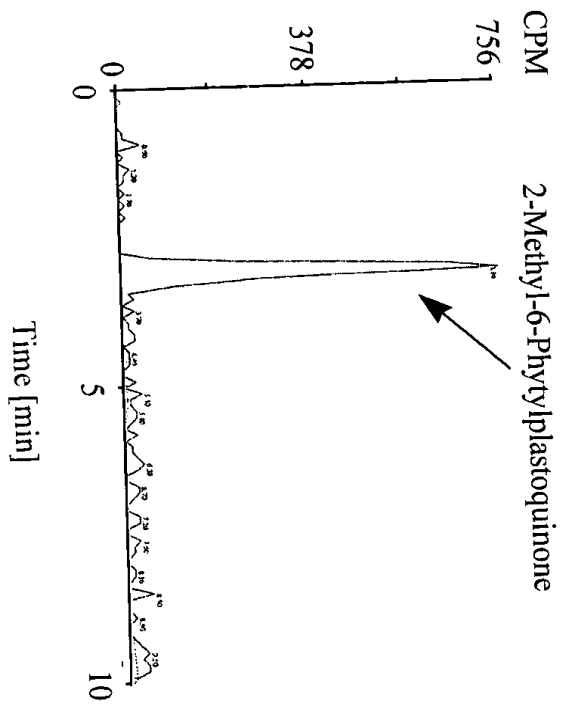
ATPT2 : \* 280 \* 300 \* 320 \* 340 \*  
 SLR1736 : LKR-FSLAALCILTIRGIVNGLFL-ERIGLVEPTITPTIT-ITLFLVFTALAEKDVPMEDGRQ-FKIQITLOIS-KON : 218  
 ATPT3 : SYP-LMKRTFWPQALGLTINMGALG-WT-AVKGS-APSTAPLYISGCWT-VYDTIYAHQKEDDVK-VKRTALRE-DNT : 213  
 SLR0926 : AYP-GAKRVFPQPLASIANMGFAVLIS--WS--AVTGDITDAW-LMGAVFWTGEDTVYAMADREDDR-IVNSAIEF-QYV : 213  
 ATPT4 : VYT-PLKOLHPINTWGAIVGALPILG--WA--AASGO-SYNSM-LPALYFWQPHFMALALCRNDYAA-GYKMLSEDP--S : 294  
 SLR1899 : VYTHMKRHTAONIVGGAAGSIPV--WA--AVTGD-SWTPW-LFALIFWTPPHFMALALMKDQYAO-VNVPMLPITAEKT : 220  
 ATPT12 : IYS-APPLKIKONGMGNFALGASISLPWMAQALFGTTPDVV-LTLLYSIAGGIAVNDKFSVEGDRA-LIQILPBAF-TET : 308  
 SLR0056 : IYS-APPLKIKONGMGNFALGASIALPWWAGHALFGTTPTIM-LTLLYSIAGGIAVNDKFSVEGDRO-LIQILPBAF-IGT : 242  
 ATPT8 : EITSSTEQRYSMDYKOKYKKTASISNSCAVAVLTGTAEVALAFEGYGRNUGAFOLIDIDIDTGTASISLKG-LSDIRH--GV : 231  
 SLR1518 : TYGPPERLGYLGLLITLITFGELAI-AAAYYSQSQSFSWMLLT-PSVFGISTAILFCSHFHVEDDL-ALKRPITRI-TKL : 223

360 \* 380 \* 400 \* 420 \* 440  
 ATPT2 : VFWTCVTLFOMAYAVAILVGATSPFINSKVISVGHVILATFWARAKSVDSLSTEITS--CYMFIWKLFYAEYLLLPK----- : 393  
 SLR1736 : VERGTLILJGCIYLAIAIWMAMAMPTAFLIVSHLCLLALFVWRSRDVHLEKTEIAS--FYQITMKLEFLEYLLYPLALWLPNS : 304  
 ATPT3 : KLMLTGCTASIGFLALSGFADLGWOYASLAASGOLGWLCTADLSSGADCS-----RKFSNKEGAILFSG-VLGRSFQ- : 407  
 SLR0926 : GEAVGIFFALTIGLFLGMILMPLIYLSLALAI--VGWV-IYIQLSAPTEP-KLY-----GOIFGQNVIIIGVLLAG-ILGWL- : 292  
 ATPT4 : GKRIAAVARNCFEWMIPLGFIAYDWGLTSSWFCLESTLTLTAATATFSFYRDRTHKA---RKMFAHSLILFLPVMSG-LHRYNSD : 379  
 SLR1899 : VSQIWWYSIVVEFESLLIVPIHQLGILYLAIALI--GGQFVYKAWQLKQAPGRDLA---RGLFKFSIFYIMLCLAMVIDSLPVT : 303  
 ATPT12 : AKMICVGAIDITLSVAGYLLASGKPYALALVALI--IPQISQFKYELKDPVKYDVK---YQASQPFVLVGI FVTAJASQH----- : 387  
 SLR0056 : AAMICVIMDVFOAGIAGYLLIVHQQLYATIVLLI--IPQITODMYFJNPLENDVK---YQASQPFVLVFGMLATGALGHAGI- : 324  
 ATPT8 : ITAPILFAEEFQREVDQVEKDPNRNDIALEYIGRSKIQARELAMHANLAALAGSLPERDNEDVKRSRALIDITHRVITRN : 320  
 SLR1518 : GSOVLTSIVSVLYLTAIGVLCHQAPWQTLIASLPNAVOLRHHVQYHDPQEVSNCK--FLAVNLHFSQMLMAVGYGWAGLG-- : 307

\* 460 \* 480 \*  
 ATPT2 : NTIF----- : 308  
 SLR1736 : ----- : -  
 ATPT3 : ----- : -  
 SLR0926 : ----- : 431  
 ATPT4 : NOQOLVEAGLTNSVSGEVKTQRRKKRVAQPPVAYASAPFPFLPAPSEYSP : 316  
 SLR1899 : --HQIWAQMGTLILG----- : -  
 ATPT12 : ----- : -  
 SLR0056 : ----- : 321  
 ATPT8 : K----- : -  
 SLR1518 : ----- : -

Figure 22 2/2

00500000 1014000



*Synechocystis* 6803 wild type      *Synechocystis* slr1736 knockout

Figure 23

0062060 : 004400



**Figure 1 Data Summary (Approximate values from charts):**

Plant line number	$\alpha$ -Tocopherol (ng/mg seed)	$\gamma$ -Tocopherol (ng/mg seed)	$\delta$ -Tocopherol (ng/mg seed)	Total tocopherol (ng/mg seed)
WT	~14	~500	~30	~530
1848	~23	~720	~85	~835
1850	~22	~680	~58	~798
1851	~18	~680	~95	~873
1853	~20	~670	~50	~770
1859	~22	~730	~58	~810
1860	~33	~800	~70	~940
1861	~30	~650	~42	~732
1862	~28	~780	~78	~936
1864	~32	~780	~75	~933
1865	~28	~700	~48	~826
1866	~24	~600	~48	~696
1868	~23	~730	~90	~813
1870	~28	~780	~62	~842
1871	~22	~730	~58	~818
1874	~22	~710	~56	~796
1876	~17	~550	~45	~630
1877	~22	~740	~68	~836
1854	~30	~820	~82	~904
1858	~23	~770	~75	~872
1863	~33	~880	~90	~993
1872	~21	~560	~58	~636
1875	~29	~780	~80	~879

Figure 24

Plant line number	ng total tocopherol/mg seed
Vect. Cont.	~550
WT	~550
1387	~550
1388	~540
1390	~530
1391	~520
1393	~180
1394	~550
1401	~420
1402	~540
1404	~550
1406	~530
1605	~560
1610	~540
1611	~580
1614	~560
1616	~540
1618	~540
1619	~570
1621	~580
1622	~530
1624	~540
1625	~680
1627	~560

Figure 25

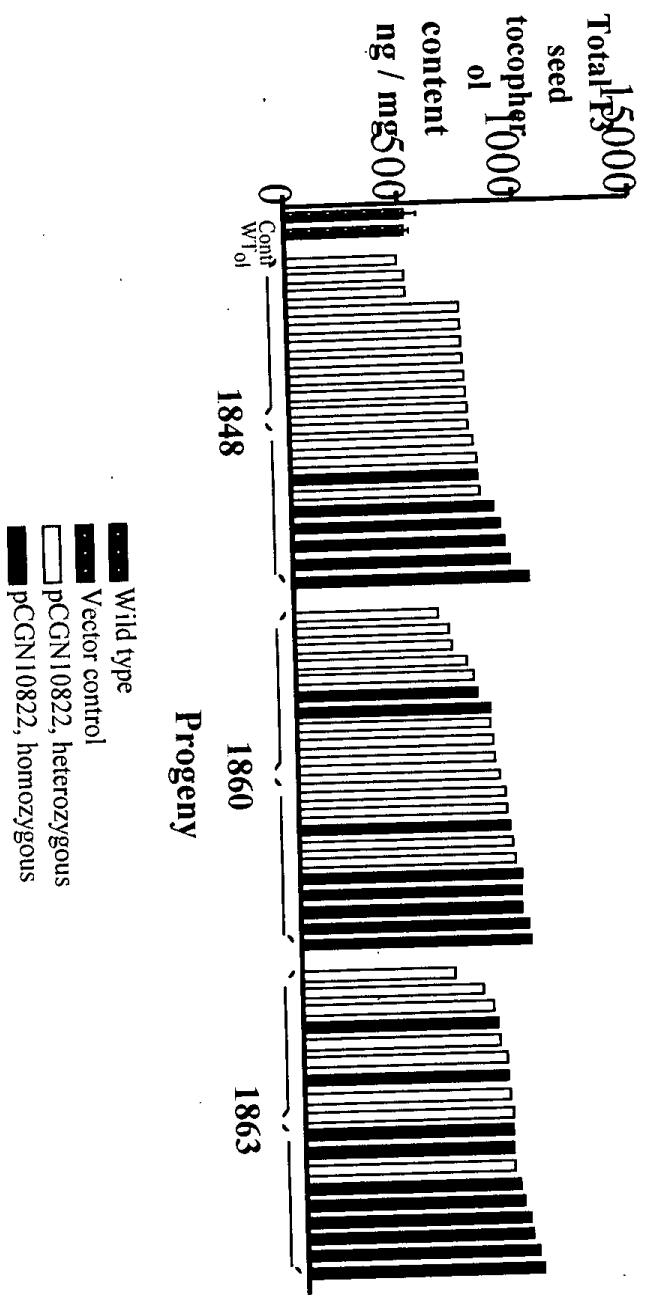


Figure 26

0069959-101400

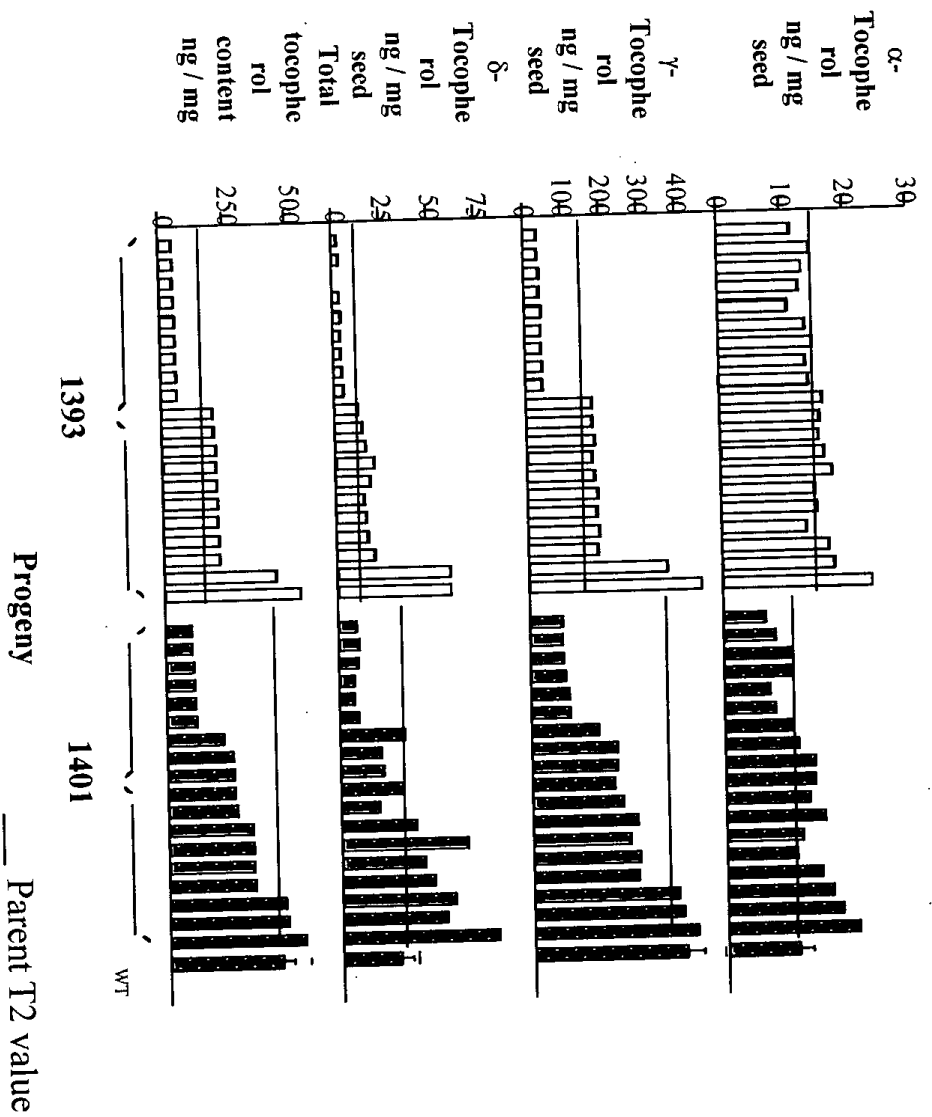


Figure 27

0069099 101400

# Total tocopherol in Napin ATPT2 Canola Seed

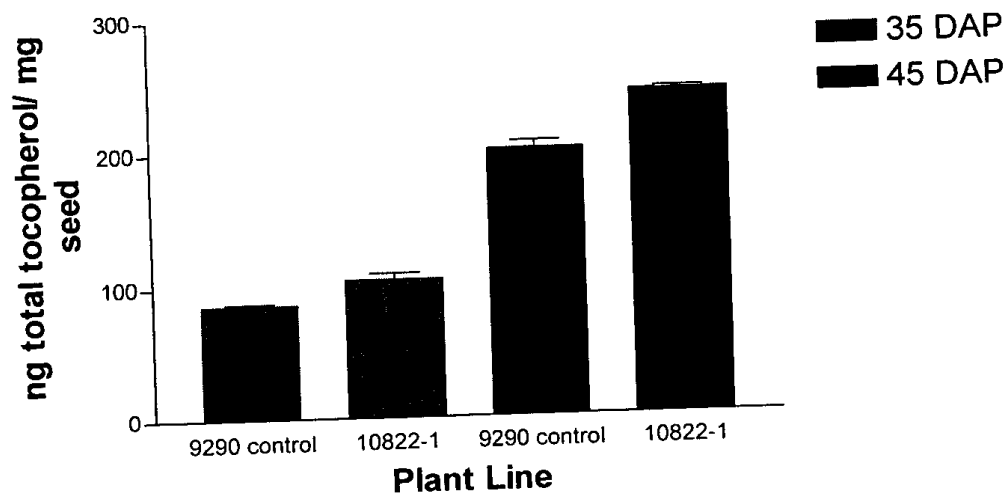


Figure 28

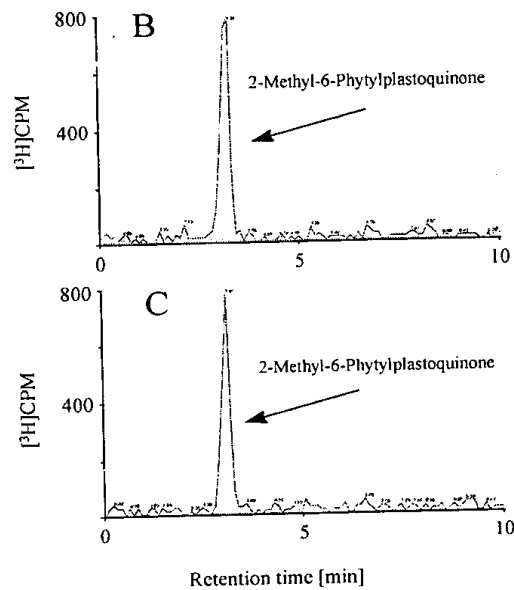
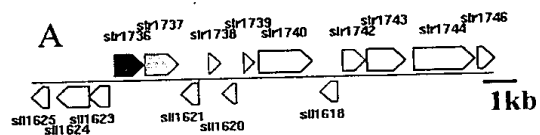


Figure 29

The figure displays four stacked chromatograms, labeled A, B, C, and D, showing the separation of tocopherols and 2,3-DMPQ. Each chromatogram has a y-axis labeled 'LU' (Luminescence Units) and an x-axis with numerical values.

- Chromatogram A:** Shows peaks for  $\alpha$ -Tocopherol,  $\beta$ -Tocopherol,  $\gamma$ -Tocopherol,  $\delta$ -Tocopherol, and Tocol. The peaks are labeled with their retention times: 2.03, 8.88, 11.08, 11.98, 13.47, 14.04, 23.75, 24.61, 25.33, and 26.88.
- Chromatogram B:** Shows peaks for 2,3-DMPQ and Tocol. The peaks are labeled with their retention times: 2.98, 3.17, 12.67, 15.85, 23.47, 24.61, 25.33, and 26.88.
- Chromatogram C:** Shows peaks for  $\alpha$ -Tocopherol and Tocol. The peaks are labeled with their retention times: 2.03, 2.98, 4.87, 8.88, 11.08, 11.98, 13.47, 23.75, 24.61, 25.33, and 26.88.
- Chromatogram D:** Shows peaks for 2,3-DMPQ and Tocol. The peaks are labeled with their retention times: 2.03, 2.98, 4.87, 11.08, 11.98, 13.47, 23.75, 24.61, 25.33, and 26.88.

Figure 30

[illegible]

Figure 31  
1/5



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ATCEA4C371+ 362 AGAGAAGAGGGAGAGTTTTGTGTTTATGTATTCTGTGGAGAATCCTGCATTTTCGGCAGAG
PIR:T04448 46 E K R E S F C F M Y S V E N P A F R Q S

Query- 11415 TTTGTCACCATTGGAAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
ATCEA4C371+ 422 TTTGTCACCATTGGAAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
PIR:T04448 66 L S P L E V A L Y G P R F T G V G A Q I

Query- 11355 TCTTGGCGCTAATGATAAATATTATGCCAATACGAACAGACTCTCACAATTTCTGGGG
ATCEA4C371+ 482 TCTTGGCGCTAATGATAAATATTATGCCAATACGAACAGACTCTCACAATTTCT
PIR:T04448 86 L G A N D K Y L C Q Y E Q D S H N F W G
ATCEA4C371+ Exon 11538 11301 Confidence: 100 100

Query- 11295 AGGTAACCTCCTTGACCCTTAAATGCTGTGTCATGACAATAAGAAATCATATCTGAGTCT
ATCEA4C371+ 537 -----
PIR:T04448 106 D -----
PIR:T04448 Exon 11609 11294 Confidence: 100 100

Query- 11235 TTTCTCTACTTCTAGTACTAATGTTTCGTTATTGTTGTTAAAGATCTAAGTCTTATCTGAA
PIR:T04448 107 -----

Query- 11175 TTTTGTTACATTTTGGTCTGTTGCTTCTCAACATGAATTTGTATATGACTTTTAAAG
PIR:T04448 107 -----

Query- 11115 ATTGCTTACCTAAAGTTTTTACTCATGCATAGATCGACATGAGCTAGTTTGGGGGAATAC
PIR:T04448 107 ----- R H E L V L G N T

Query- 11055 TTTTAGTGTGTGCCAGGCGCAAAGGCTCCAAACAGGAGGTTCCACCAGAGGTTCTCAC
PIR:T04448 116 F S A V P G A K A P N K E V P P E
PIR:T04448 Exon 11083 11004 Confidence: 96 100

Query- 10995 TCCTCCCTTGTGTTACTTTGTTATCTGTTAAATAGTTTCCAATTGTATCCGGATAGT
PIR:T04448 133 -----

Query- 10935 GTTCTACTTCTCCTTGTAAGAAATCTCAAGTTTTTGTACTCTTGCTATTCTCTTGGATG
PIR:T04448 133 -----

Query- 10875 TTGATTGTAAAGCATGTCGTTTTATTGTAGGAATTTAACAGAAGAGTGTCCGAAGGGTT
PIR:T04448 133 ----- E F N R R V S E G F

Query- 10815 CCAAGCTACTCCATTTTGGCATCAAGGTCACATTGCGATGATGGCCGGTAATTATATGA
PIR:T04448 143 Q A T P F W H Q G H I C D D G R
PIR:T04448 Exon 10844 10768 Confidence: 100 100

Query- 10755 TTCTATGCACAACAAGAATTCACTATATTATAAATATTGGATATTGAGTATTTTGTGTA
PIR:T04448 159 -----

Query- 10695 AAATTTCTGTGTTTAAATCTGACTTGACTTGTTTGTGTCAGTACTGACTATCGGAAACTG
PIR:T04448 159 ----- T D Y A E T V

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Figure 31  
2/5

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Query-      10635 TGAATCTGCTCGTTGGGAGTATAGTACTCGTCCCGTTTACGGTTGGGGTGATGTTGGGG
PIR:T04448      166   K S A R W E Y S T R P V Y G W G D V G A

Query-      10575 CCAAACAGAAGTCAACTGCAGGCTGGCCTGCAGCTTTTCCTGTAATTTAGACCTCATTGGC
PIR:T04448      186   K Q K S T A G W P A A F P V F E P H W Q

Query-      10515 AGATATGCATGGCAGGAGGCCTTTCCACAGGTGTGAGCTTTGCTTGATTGACTTAAAGTT
PIR:T04448      206   I C M A G G L S T G
PIR:T04448      Exon   10655   10486   Confidence: 96 100

Query-      10455 AATAAATAGACGGTTAAGTTTACTTGCCTAGTACTAACAGAAAATTAAGAAAGAAACCAC
PIR:T04448      216

Query-      10395 CCTCTTTCTATCAGCAGAACTGCATTATTGTAGTTCTTATTTTTTCTCTTGATTATTCAGG
PIR:T04448      216

Query-      10335 GTGGATAGAATGGGGCGGTGAAAGGTTTGAGTTTCGGGATGCACCTTCTTATTCAGAGAA
PIR:T04448      216   W I F W G G E R F E F R D A P S Y S E K

Query-      10275 GAATTGGGGTGGAGGCTTCCCAAGAAAATGGTTTGGGTAAACATTTTCATCCTTTTGCT
PIR:T04448      236   N W G G G F P R K W F W
PIR:T04448      Exon   10336   10239   Confidence: 96 100

Query-      10215 ACATTTCTTGTTGCAGACTTTAGTTAGCTAGTGGACCTGTGTATACACCCACATGTAGTA
PIR:T04448      248

Query-      10155 TACTTGTTTGATAGCTTTATTGTGCAATGTCTCTTTACAGGTCCAGTGTAATGTCTTTGA
PIR:T04448      248                               V Q C N V F E

Query-      10095 AGGGGCAACTGGAGAAGTTGCTTTAACCAGGAGGTGGCGGGTTGAGGCAATTGCCTGGATT
PIR:T04448      255   G A T G E V A L T A G G G L R Q L P G L

Query-      10035 GACTGAGACCTATGAAATGCTGCACTGGTATGCACTTATAAGATCTTCTTAAGCAATGA
PIR:T04448      275   T E T Y E N A A L
PIR:T04448      Exon   10115   10008   Confidence: 100 100

Query-      9975  CAGTGAGTATTAGAAGGCAGATAGTTTACAAAAGCTCTGGGCCCTTGTAATCTGCAGGT
PIR:T04448      284                               V

Query-      9915  TTGTGTACACTATGATGGAAAAATGTACGAGTTTGTTCTTGGAAATGGTGTGTAGATG
PIR:T04448      285   C V H Y D G K M Y E F V P W N G V V R W
GSDB:S:495-      532                               tagatg

Query-      9855  GGAAATGTCTCCCTGGGG TTATTGGTATATAACTGCAGAGAACGAAAACCATGTGGTAA
PIR:T04448      305   E M S P W G Y W Y I T A E N E N H V
GSDB:S:495-      526   ggaaat tctccctgggggttatggatataaactgcagagaaNcgNaaaccatgtg
PIR:T04448      Exon   9917   9801   Confidence: 100 100
GSDB:S:495-      Exon   9861   9801   Confidence: 93 93

Query-      9796  ATTTGTTTACTAGTTTCATTACGTTTACTTTTGACATCATATCATTCCCTTATGGCTA

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Figure 31  
3/5

```

323
PIR:T04448
GSDB:S:495-
471
Query-
9736 GATTCCAACACCCGATGAATGCTTGTGACAGGTGGAAC TAGAGGCAAGACAAATGAAG
V E L E A R T N E A
PIR:T04448
323
gtggaactagaggcNagaacaatgaag
GSDB:S:495-
471
Query-
9676 CGGGTACACCTCTGCGTGTCTTACCACAGAAGTTGGGCTAGCTACGGCTTG CAGAGATA
G T P L R A P T T E V G L A T A C R D S
PIR:T04448
333
cgggtaacacctctgctgtctctaccacagaagttgggctagctacggcttg cagagata
GSDB:S:495-
443
Query-
9616 GTTGTACGGTGAATTGAAGTTGCAGATATGGGAACGGCTATATGATGGAAGTAAAGGCA
C Y G E L K L Q I W E R L Y D G S K G K
PIR:T04448
353
gttggttacggtgaattgaagttgcagatatgggaacggctatatgatggaagtaaaggca
GSDB:S:495-
383
Query-
9556 AGGTATGTATGCTAATGTGATCCAATCCCTGTAGTTAAAGTCTTAACAAATCCTAAGGC
L K V L T N P K A
PIR:T04448
373
323 ag
Exon 9704 9555 Confidence: 100 100
Exon 9704 9555 Confidence: 98 100
GSDB:S:495-
Query-
9496 AGTGAAAGAAGATTATGAACGTTTGTATGGTTAACAATGATGCAGGTGATATTAGAGAC
V K E D Y E R L L W L T M M Q V I L E T
PIR:T04448
382
gtgatattagagac
GSDB:S:495-
321
Query-
9436 AAAGAGCTCAATGGCAGCAGTGGAGATAGGAGGAGGACCGTGGTTTGGGACATGGAAGG
K S S M A A V E I G G G P W F G T W K G
PIR:T04448
402
aaagagctcaatggcaNcagtgagataggaggaggaccgtggtttgggacatggaag
GSDB:S:495-
307
Query-
9376 AGATACGAGCAACACGCCCCGAGCTACTAAAACAGGCTCTTCAGGTCCCAATTGGATCTTGA
D T S N T P E L L K Q A L Q V P L D L E
PIR:T04448
422
agatacgagcaacacgccccgagctactaaaacaggctcttcagggtcccatggatcttga
GSDB:S:495-
247
Query-
9316 AAGCGCCTTAGGTTTGGTCCCTTCTTCAAGCCACCGGGTCTG TAA CATTGATGAGTGT
S A L G L V P F F K P P G L
PIR:T04448
442
aagcgcttaggtttgggtccctttcttcaagccacgggtctgtaacattgatgagtggt
GSDB:S:495-
187
Exon 9522 9274 Confidence: 100 100
PIR:T04448
Query-
9256 TTGTTTGTGTGATAGAGACCCATGTGATGAATGAAGCCTTAGTCATGTCTATTGCTAGCTTG
T G T T T G T G A T A G A G A C C C A T G T G A T G A A T G A A G C C T T A G T C A T G T C A T T G C T A G C T T G
PIR:T04448
456
ttgtttgttgatagagaccatgtgatgaatgaagccttagtcatgtcattgctagcttc
GSDB:S:495-
127
Query-
9196 ACTATTATGTATGTATGATTTTAGTTTCGTTTCGGTCTTGTGGTAAATGATACGGGCCAGT
a c t a t t a t g t a t g t a t g a t t t a g t t c g t t c g g t c c t t g t g g t a a a t g a t a c g g g c c a g t
PIR:T04448
67
GSDB:S:495-
Query-
9136 GTAAAGTCTAGTTCAATAAAAGCCTTGAGTCGCATAAATTCAATTTCAAATTGCATC
g t a a a g t
GSDB:S:495-
7
Exon 9450 9130 Confidence: 98 100
GSDB:S:495-

```

Figure 31  
4/5

PIR:T04448 sPIR:T04448 shypothetical protein F4D11.30 - Arabidopsis thaliana;  
 -1512218584.1 (AL022537) putative protein [Arabidopsis thaliana]\_F4

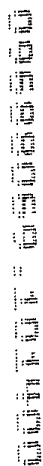
PIR:T04448 sPIR-T04448 shypoetical protein F4D11.30 - Arabidopsis thaliana;  
g3063693|emb|CAA18584.1 (AL022537) putative protein [Arabidopsis thaliana]\_F4D11.30

g3063693|emb|CAA18584.1 (AL022537) putative protein [Arabidopsis thaliana]  
 GSDB:S:4955486|AI995392|AI995392|701673779 A. thaliana, Columbia Col-0, inflorescence-  
 1 Arabidopsis thaliana cDNA clone 701673779, mRNA sequence.

Figure 1 consists of 12 histograms arranged in two rows of six. The top row is labeled '1000 iterations' and the bottom row is labeled '10000 iterations'. Each histogram shows the frequency of the number of non-zero elements in the vector of the first 1000 iterations of the algorithm. The x-axis for each histogram is labeled 'Number of non-zero elements' and the y-axis is labeled 'Frequency'. The histograms are labeled with their respective iteration counts: 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000. The distributions are centered around 1000 for the top row and 10000 for the bottom row.

Figure 32

Figure 33

[illegible]

slr1737\_SYNSP\_S74814\_  
slr1737\_ARATH\_T04448\_  
CFI\_ARATH\_P41088\_

---DWGLTEENLSKKT---VPE---  
TWKGDTSNTPELLKQALQVPLDLESALGLVPFFKPPGL  
---EKLAKEN---

Figure 35